45. The method of claim **44**, wherein the random or partially random sequences comprise a length from about 5 nucleotides to about 10 nucleotides.

46. The method of claim **44**, wherein the identifier tags are double-stranded sequences.

47. The method of claim **39**, further comprising purifying a plurality of cypher-target nucleic acid complexes prior to sequencing, wherein the purified cypher-target nucleic acid complexes comprise nucleic acid molecules from specific genomic regions.

48. The method of claim **39**, wherein prior to sequencing, the method further comprises amplifying each strand of the cypher-target nucleic acid complexes to produce a set of copies of original first strands of the cypher-target nucleic acid complexes and a set of copies of complementary original second strands of the cypher-target nucleic acid complexes.

49. The method of claim **39**, wherein prior to comparing the first-strand sequencing reads with the second-strand sequencing reads, the method comprises grouping sequencing reads based on (i) the identifier tag sequences and (ii) sequence information from the double-stranded DNA molecules.

50. The method of claim **39**, wherein each of the error-corrected sequences has only nucleotide bases at which the majority of first strand sequencing reads and second strand sequencing reads are in agreement.

51. The method of claim **50**, wherein the method comprises calculating a mutation frequency among the plurality of double-stranded DNA molecules.

52. The method of claim **51**, wherein the mutations are transition mutations.

53. The method of claim **50**, wherein a sequence difference between the error-corrected sequence and the reference sequence is identified as a true mutation.

54. The method of claim **53**, wherein the true mutation is a substitution or insertion mutation type.

55. The method of claim **53**, wherein the true mutation is a transition mutation.

56. The method of claim **50**, wherein the error-corrected sequences map to the reference sequence, and the method further comprises identifying a distribution of mutations in the double-stranded DNA molecules.

57. The method of claim **54**, wherein the error-corrected sequences map to the reference sequence, and the method further comprises identifying a distribution of mutation types in the double-stranded DNA molecules.

58. The method of claim **39**, wherein the error corrected sequence is generated by distinguishing erroneous nucleotides in one strand that lack a matched base change in the complementary strand, and wherein the erroneous nucleotides are the result of systematic or biological errors in one strand.

59. The method of claim **39**, wherein the method comprises determining a genomic distribution of mutations with respect to the reference sequence.

60. A method of identifying effects of DNA damaging compounds, the method comprising:

(a) providing a sample comprising a plurality of double-stranded DNA molecules from a patient that has been treated with a compound;

(b) preparing a sequencing library from the sample by ligating cypher polynucleotides to the double-stranded DNA molecules to form double-stranded cypher-target nucleic acid complexes, wherein the cypher polynucleotides comprise identifier tags selected from a plurality of distinct identifier tag sequences;

(c) for each cypher-target nucleic acid complex among a plurality of the cypher-target nucleic acid complexes, generating a set of copies of a first strand of the cypher-target nucleic acid complex and a set of distinct yet related copies of a complementary second strand of the cypher-target nucleic acid complex;

(d) sequencing one or more copies of the first and complementary second strands to produce a plurality of first-strand sequencing reads and a plurality of distinct yet related second-strand sequencing reads;

(e) for each cypher-target nucleic acid complex among a plurality of the cypher-target nucleic acid complexes, comparing the first-strand sequencing reads with the second-strand sequencing reads to identify nucleotides in the first strand that have a corresponding complementary nucleotide in the second strand;

(f) comparing an error-corrected sequence generated from the first strand sequencing reads and second strand sequencing reads to a reference sequence to determine one or more of a mutation, a genomic distribution of mutations, a mutation frequency, sequence heterogeneity, or DNA damage; and

(g) based on the comparing step, identifying DNA damage from the compound.

61. The method of claim **60**, wherein the error corrected sequence is generated by distinguishing erroneous nucleotides in one strand that lack a matched base change in the complementary strand, and wherein the erroneous nucleotides are the result of systematic or biological errors in one strand.

62. The method of claim **60**, wherein step (a) further comprises providing a plurality of samples from a plurality of patients treated with the compound.

63. The method of claim **60**, further comprising purifying a plurality of cypher-target nucleic acid complexes prior to sequencing, wherein the purified cypher-target nucleic acid complexes comprise nucleic acid molecules from specific genomic regions, and wherein the specific genomic regions comprise mutations common to most cells of a tumor.

64. The method of claim **60**, wherein the double-stranded DNA molecules comprise a deaminated cytosine.

65. The method of claim **64**, wherein the method further comprises enzymatically treating the double-stranded DNA molecules to repair damaged ends thereof prior to the ligating.

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